

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/382,096DATE: 01/21/2000
TIME: 13:54:21

Input Set: I382096.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Outtrup, Helle
 2 Nielsen, Bjarne Roenfeldt
 3 Hedegaard, Lisbeth
 4 Andersen, Jens Toenne
 5 <120> TITLE OF INVENTION: Alkaline Bacillus Amylase
 6 <130> FILE REFERENCE: 5442.400-US
 7 <140> CURRENT APPLICATION NUMBER: US/09/382,096
 8 <141> CURRENT FILING DATE: 1999-08-24
 9 <150> EARLIER APPLICATION NUMBER: 0228/98
 10 <151> EARLIER FILING DATE: 1998-02-18
 11 <150> EARLIER APPLICATION NUMBER: 60/146,297
 12 <151> EARLIER FILING DATE: 1998-02-27
 13 <150> EARLIER APPLICATION NUMBER: 09/249,558
 14 <151> EARLIER FILING DATE: 1999-02-12
 15 <160> NUMBER OF SEQ ID NOS: 4
 16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 17 <210> SEQ ID NO 1
 18 <211> LENGTH: 1646
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Bacillus sp.
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (1)...(1646)
 24 <221> NAME/KEY: sig_peptide
 25 <222> LOCATION: (1)...(93)
 26 <221> NAME/KEY: mat_peptide
 27 <222> LOCATION: (94)...(1646)
 28 <400> SEQUENCE: 1

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30	Met Gln Asn Thr Ala Lys Asn Ser Ile Trp Gln Arg Val Arg His Ser	
31	-30 -25 -20	
32	gcc att gcc tta tcc gct ctc agt tta tcc ttt ggc ctg cag gcc agc	96
33	Ala Ile Ala Leu Ser Ala Leu Ser Leu Ser Phe Gly Leu Gln Ala Ser	
34	-15 -10 -5 1	
35	gag tta cca caa att cca cca cag cag gtg aac aac acc atg tac cag	144
36	Glu Leu Pro Gln Ile Pro Pro Gln Gln Val Asn Asn Thr Met Tyr Gln	
37	5 10 15	
38	gca ttt tat tgg gat gcc tac cct ggc ctt tgg gcc aat tta ccg gcc	192
39	Ala Phe Tyr Trp Asp Ala Tyr Pro Gly Leu Trp Ala Asn Leu Pro Ala	
40	20 25 30	
41	atg gcg gcc cct ttg gcc gag cgt ggc att acc tcg atg tgg ttg ccg	240
42	Met Ala Ala Pro Leu Ala Glu Arg Gly Ile Thr Ser Met Trp Leu Pro	
43	35 40 45	
44	ccc gcc gcc aaa ggc atg aat ggt act ttc agt gtc ggt tac gat gta	288

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/382,096DATE: 01/21/2000
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45	Pro Ala Ala Lys Gly Met Asn Gly Thr Phe Ser Val Gly Tyr Asp Val			
46	50	55	60	65
47	tac gat ttc tgg gat ctg ggc gag ttt aac caa aaa ggc acc acc ggc		336	
48	Tyr Asp Phe Trp Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Thr Ala			
49	70	75	80	
50	acc cgt tac ggt act cgt cag cag ctg caa caa gca ctg agt gct ctg		384	
51	Thr Arg Tyr Gly Thr Arg Gln Gln Leu Gln Gln Ala Leu Ser Ala Leu			
52	85	90	95	
53	gac caa ctg ggt att cag gcc tat ttt gat gtg gtg ttt aac cac cgc		432	
54	Asp Gln Leu Gly Ile Gln Ala Tyr Phe Asp Val Val Phe Asn His Arg			
55	100	105	110	
56	atg ggc gcc gat gca cag gag aat att cct ggc ttt ggc ctg gcc tgg		480	
57	Met Gly Ala Asp Ala Gln Glu Asn Ile Pro Gly Phe Gly Leu Ala Trp			
58	115	120	125	
59	acc gag tat cat ctg caa ggt cgt cag gcg cat tat acc cag caa aac		528	
60	Thr Glu Tyr His Leu Gln Gly Arg Gln Ala His Tyr Thr Gln Gln Asn			
61	130	135	140	145
62	tgg ggc tac ttg tgg cac gac ttt gac tgg aac tgg acc gcg ttt aat		576	
63	Trp Gly Tyr Leu Trp His Asp Phe Asp Trp Asn Trp Thr Ala Phe Asn			
64	150	155	160	
65	ggc tcc gac aat cag ctc tac ccc ggc aaa tgg tgg ggc aat acc ttc		624	
66	Gly Ser Asp Asn Gln Leu Tyr Pro Gly Lys Trp Trp Gly Asn Thr Phe			
67	165	170	175	
68	cac ttc cct tat ttg atg ggt gag gat gtc gat tac aac cgc ttt gaa		672	
69	His Phe Pro Tyr Leu Met Gly Glu Asp Val Asp Tyr Asn Arg Phe Glu			
70	180	185	190	
71	gtg cag cag gaa atg aaa gcc tgg ggc gag tgg atc atc aac agc gtt		720	
72	Val Gln Gln Glu Met Lys Ala Trp Gly Glu Trp Ile Ile Asn Ser Val			
73	195	200	205	
74	ggc ttt agc ggc ttt cgg atg gat gcc atc gcc cat gtc gat acc gat		768	
75	Gly Phe Ser Gly Phe Arg Met Asp Ala Ile Ala His Val Asp Thr Asp			
76	210	215	220	225
77	ttt acc cgt gac tgg atc aat cac gtc cag tgg gcc acc agt gag gat		816	
78	Phe Thr Arg Asp Trp Ile Asn His Val Gln Trp Ala Thr Ser Glu Asp			
79	230	235	240	
80	gtg ttc ttt gtc gct gaa gcc tgg gtc agt gat atc aac ggc tat ctg		864	
81	Val Phe Phe Val Ala Glu Ala Trp Val Ser Asp Ile Asn Gly Tyr Leu			
82	245	250	255	
83	gat gca gtc aat acg ccg cat ttg cgc gct ttt gat ttc aat ttg cgc		912	
84	Asp Ala Val Asn Thr Pro His Leu Arg Ala Phe Asp Phe Asn Leu Arg			
85	260	265	270	
86	gaa gac ttc gtt gct tta agc agc ggt agc aaa gac atg cgt tgg tgg		960	
87	Glu Asp Phe Val Ala Leu Ser Ser Gly Ser Lys Asp Met Arg Trp Trp			
88	275	280	285	
89	ggc ggt ctg gtc aat agc cag cac cgt gat cgg ggc gtc act ttt gtc		1008	
90	Gly Gly Leu Val Asn Ser Gln His Arg Asp Arg Ala Val Thr Phe Val			
91	290	295	300	305
92	gat aac cac gat acc agc cgg gcc ggc aac cct tat ggc atg ccg cag		1056	
93	Asp Asn His Asp Thr Ser Arg Ala Gly Asn Pro Tyr Gly Met Pro Gln			
94	310	315	320	

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/382,096DATE: 01/21/2000
TIME: 13:54:21

Input Set: I382096.RAW

95	gtg atc aac tac aag aac cag gcc tac gct tac att ctg ttg cgt gag	1104
96	Val Ile Asn Tyr Lys Asn Gln Ala Tyr Ala Tyr Ile Leu Leu Arg Glu	
97	325 330 335	
98	cat ggg gtg ccg act gtg ttt gcc cgc gat tac gac gaa ttt ggc atg	1152
99	His Gly Val Pro Thr Val Phe Ala Arg Asp Tyr Asp Glu Phe Gly Met	
100	340 345 350	
101	gct cca acg ctg gat aaa ttg att gag gct cgc cgc tac ttt gct tat	1200
102	Ala Pro Thr Leu Asp Lys Leu Ile Glu Ala Arg Arg Tyr Phe Ala Tyr	
103	355 360 365	
104	ggt cct ggc cat gag tac tcc ggc aat acc gag gcc gtc tac gcc tat	1248
105	Gly Pro Gly His Glu Tyr Ser Gly Asn Thr Glu Ala Val Tyr Ala Tyr	
106	370 375 380 385	
107	gtg cgc gaa ggg ctt agc act gtg ccg ggt acc ggt ctg gtg atg ctg	1296
108	Val Arg Glu Gly Leu Ser Thr Val Pro Gly Thr Gly Leu Val Met Leu	
109	390 395 400	
110	ata tcg ggt cga aac tgg ggt cag cag tcg ttc acc atc aac agc	1344
111	Ile Ser Gly Arg Asn Trp Gly Gly Gln Gln Ser Phe Thr Ile Asn Ser	
112	405 410 415	
113	cac cag ccg aat acc acc ttt tac gat tat acc ggc aat gtt agc ggc	1392
114	His Gln Pro Asn Thr Phe Tyr Asp Tyr Thr Gly Asn Val Ser Gly	
115	420 425 430	
116	acg gtg acc acc aat gcg cag ggc tat ggc agc ttc ccg gtc act atg	1440
117	Thr Val Thr Asn Ala Gln Gly Tyr Gly Ser Phe Pro Val Thr Met	
118	435 440 445	
119	acg gaa agt acc ggt tgg tca gtc tgg gta cca caa tcc aat ggt ggc	1488
120	Thr Glu Ser Thr Gly Trp Ser Val Trp Val Pro Gln Ser Asn Gly Gly	
121	450 455 460 465	
122	act cag ccg gga tcc att acc ctg cgg atg acc aag gat gtt ggc tat	1536
123	Thr Gln Pro Gly Ser Ile Thr Leu Arg Met Thr Lys Asp Val Gly Tyr	
124	470 475 480	
125	ggc ttt tcg ttg ttc acc ggc agc agt gct gaa ctg acc aac tgg	1584
126	Gly Phe Ser Leu Phe Phe Thr Gly Ser Ser Ala Glu Leu Thr Asn Trp	
127	485 490 495	
128	ggc ggc ggt att gaa ggc acc tgg aca tcc ggt aat gtc tgg gaa gtg	1632
129	Gly Gly Ile Glu Gly Thr Trp Thr Ser Gly Asn Val Trp Glu Val	
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131	acc atc ccg gat cc	1646
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133	515	
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140	<222> LOCATION: (1)...(31)	
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144	Ala Ile Ala Leu Ser Ala Leu Ser Leu Ser Phe Gly Leu Gln Ala Ser	

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/382,096DATE: 01/21/2000
TIME: 13:54:21

Input Set: I382096.RAW

145	-15	-10	-5	1												
146	Glu	Leu	Pro	Gln	Ile	Pro	Pro	Gln	Gln	Val	Asn	Asn	Thr	Met	Tyr	Gln
147					5					10					15	
148	Ala	Phe	Tyr	Trp	Asp	Ala	Tyr	Pro	Gly	Leu	Trp	Ala	Asn	Leu	Pro	Ala
149						20				25					30	
150	Met	Ala	Ala	Pro	Leu	Ala	Glu	Arg	Gly	Ile	Thr	Ser	Met	Trp	Leu	Pro
151						35				40				45		
152	Pro	Ala	Ala	Lys	Gly	Met	Asn	Gly	Thr	Phe	Ser	Val	Gly	Tyr	Asp	Val
153						50				55			60		65	
154	Tyr	Asp	Phe	Trp	Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Thr	Ala
155						70				75				80		
156	Thr	Arg	Tyr	Gly	Thr	Arg	Gln	Gln	Leu	Gln	Gln	Ala	Leu	Ser	Ala	Leu
157						85				90				95		
158	Asp	Gln	Leu	Gly	Ile	Gln	Ala	Tyr	Phe	Asp	Val	Val	Phe	Asn	His	Arg
159						100				105				110		
160	Met	Gly	Ala	Asp	Ala	Gln	Glu	Asn	Ile	Pro	Gly	Phe	Gly	Leu	Ala	Trp
161						115				120				125		
162	Thr	Glu	Tyr	His	Leu	Gln	Gly	Arg	Gln	Ala	His	Tyr	Thr	Gln	Gln	Asn
163						130				135			140		145	
164	Trp	Gly	Tyr	Leu	Trp	His	Asp	Phe	Asp	Trp	Asn	Trp	Thr	Ala	Phe	Asn
165						150				155				160		
166	Gly	Ser	Asp	Asn	Gln	Leu	Tyr	Pro	Gly	Lys	Trp	Trp	Gly	Asn	Thr	Phe
167						165				170				175		
168	His	Phe	Pro	Tyr	Leu	Met	Gly	Glu	Asp	Val	Asp	Tyr	Asn	Arg	Phe	Glu
169						180				185				190		
170	Val	Gln	Gln	Glu	Met	Lys	Ala	Trp	Gly	Glu	Trp	Ile	Ile	Asn	Ser	Val
171						195				200				205		
172	Gly	Phe	Ser	Gly	Phe	Arg	Met	Asp	Ala	Ile	Ala	His	Val	Asp	Thr	Asp
173						210				215			220		225	
174	Phe	Thr	Arg	Asp	Trp	Ile	Asn	His	Val	Gln	Trp	Ala	Thr	Ser	Glu	Asp
175						230				235				240		
176	Val	Phe	Phe	Val	Ala	Glu	Ala	Trp	Val	Ser	Asp	Ile	Asn	Gly	Tyr	Leu
177						245				250				255		
178	Asp	Ala	Val	Asn	Thr	Pro	His	Leu	Arg	Ala	Phe	Asp	Phe	Asn	Leu	Arg
179						260				265				270		
180	Glu	Asp	Phe	Val	Ala	Leu	Ser	Ser	Gly	Ser	Lys	Asp	Met	Arg	Trp	Trp
181						275				280				285		
182	Gly	Gly	Leu	Val	Asn	Ser	Gln	His	Arg	Asp	Arg	Ala	Val	Thr	Phe	Val
183						290				295			300		305	
184	Asp	Asn	His	Asp	Thr	Ser	Arg	Ala	Gly	Asn	Pro	Tyr	Gly	Met	Pro	Gln
185						310				315				320		
186	Val	Ile	Asn	Tyr	Lys	Asn	Gln	Ala	Tyr	Ala	Tyr	Ile	Leu	Leu	Arg	Glu
187						325				330				335		
188	His	Gly	Val	Pro	Thr	Val	Phe	Ala	Arg	Asp	Tyr	Asp	Glu	Phe	Gly	Met
189						340				345				350		
190	Ala	Pro	Thr	Leu	Asp	Lys	Leu	Ile	Glu	Ala	Arg	Arg	Tyr	Phe	Ala	Tyr
191						355				360				365		
192	Gly	Pro	Gly	His	Glu	Tyr	Ser	Gly	Asn	Thr	Glu	Ala	Val	Tyr	Ala	Tyr
193						370				375			380		385	
194	Val	Arg	Glu	Gly	Leu	Ser	Thr	Val	Pro	Gly	Thr	Gly	Leu	Val	Met	Leu

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/382,096DATE: 01/21/2000
TIME: 13:54:21

Input Set: I382096.RAW

195	390	395	400	
196	Ile Ser Gly Arg Asn Trp Gly Gly Gln Gln Ser Phe Thr Ile Asn Ser			
197	405	410	415	
198	His Gln Pro Asn Thr Thr Phe Tyr Asp Tyr Thr Gly Asn Val Ser Gly			
199	420	425	430	
200	Thr Val Thr Thr Asn Ala Gln Gly Tyr Gly Ser Phe Pro Val Thr Met			
201	435	440	445	
202	Thr Glu Ser Thr Gly Trp Ser Val Trp Val Pro Gln Ser Asn Gly Gly			
203	450	455	460	465
204	Thr Gln Pro Gly Ser Ile Thr Leu Arg Met Thr Lys Asp Val Gly Tyr			
205	470	475	480	
206	Gly Phe Ser Leu Phe Phe Thr Gly Ser Ser Ala Glu Leu Thr Asn Trp			
207	485	490	495	
208	Gly Gly Gly Ile Glu Gly Thr Trp Thr Ser Gly Asn Val Trp Glu Val			
209	500	505	510	
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211	515			
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213	<211> LENGTH: 1764			
214	<212> TYPE: DNA			
215	<213> ORGANISM: Bacillus sp.			
216	<220> FEATURE:			
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225	Met Gln Asn Thr Ala Lys Asn Ser Ile Trp Gln Arg Val Arg His Ser			
226	-30	-25	-20	
227	gcc att gcc tta tcc gct ctc agt tta tcc ttt ggc ctg cag gcc agc		96	
228	Ala Ile Ala Leu Ser Ala Leu Ser Leu Ser Phe Gly Leu Gln Ala Ser			
229	-15	-10	-5	1
230	gag tta cca caa att cca cca cag cag gtg aac aac acc atg tac cag		144	
231	Glu Leu Pro Gln Ile Pro Pro Gln Gln Val Asn Asn Thr Met Tyr Gln			
232	5	10	15	
233	gca ttt tat tgg gat gcc tac cct ggc ctt tgg gcc aat tta ccg gcc		192	
234	Ala Phe Tyr Trp Asp Ala Tyr Pro Gly Leu Trp Ala Asn Leu Pro Ala			
235	20	25	30	
236	atg gcg gcc cct ttg gcc gag cgt ggc att acc tcg atg tgg ttg ccg		240	
237	Met Ala Ala Pro Leu Ala Glu Arg Gly Ile Thr Ser Met Trp Leu Pro			
238	35	40	45	
239	ccc gcc gcc aaa ggc atg aat ggt act ttc agt gtc ggt tac gat gta		288	
240	Pro Ala Ala Lys Gly Met Asn Gly Thr Phe Ser Val Gly Tyr Asp Val			
241	50	55	60	65
242	tac gat ttc tgg gat ctg ggc gag ttt aac caa aaa ggc acc acc gcc		336	
243	Tyr Asp Phe Trp Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Thr Ala			
244	70	75	80	

PAGE: 6

VERIFICATION SUMMARY
PATENT APPLICATION US/09/382,096

DATE: 01/21/2000
TIME: 13:54:21

Input Set: I382096.RAW

Line ? Error/Warning

Original Text

333 W Line data has been corrected

Thr Asn Leu His Pro Ser Phe Asn Gly Gly P